Supplementary Table S3. *S*-Guanylated Proteins in Solubilized Mitochondria Treated *In Vitro* with 8-Nitro-cGMP as Identified by 2D-PAGE and LC-MS/MS

Spot no.	Acc no.[a]	Protein name	Sequence coverage (%)	No. of matched peptides	Mascot score	Mw[b]	pI[c]
1	Q66HD0	Endoplasmin	33	26	1106	92713	4.72
3	Q3KR86	Mitochondrial inner membrane protein (fragment)	5	4	41	67135	5.57
5	P06761	78 kDa glucose-regulated protein	56	29	1445	72302	5.07
6	P06761	78 kDa glucose-regulated protein	10	2	53	72302	5.07
7	P48721	Stress-70 protein, mitochondrial	40	23	1030	73812	5.97
7	P48679	Prelamin-A/C	19	14	302	74279	6.54
7	P63018	Heat shock cognate 71 kDa protein	10	7	54	70827	5.37
8	P70615	Lamin-B1	55	30	1897	66566	5.16
8	P55063	Heat shock 70 kDa protein 1-like	3	2	45	70505	5.91
9	P68370	Tubulin alpha-1A chain	5	2	42	50104	4.94
10	P61980	Heterogeneous nuclear ribonucleoprotein K	27	12	387	50944	5.39
10	P63039	60 kDa heat shock protein, mitochondrial	16	6	34	60917	5.91
11	P31000	Vimentin	22	10	89	53700	5.06
11	P18418	Calreticulin	24	10	87	47966	4.33
13	Q9R064	Golgi reassembly-stacking protein 2	12	5	79	47191	4.84
13	P31000	Vimentin	17	8	76	53700	5.06
14	P04785	Protein disulfide-isomerase	53	26	747	56916	4.82
14	P69897	Tubulin beta-5 chain	40	14	224	49639	4.78
15	P69897	Tubulin beta-5 chain	55	18	1404	49639	4.78
15	Q6P9T8	Tubulin beta-4B chain	49	17	1139	49769	4.79

15	P85108	Tubulin beta-2A chain	55	18	1098	49875	4.78
15	P31000	Vimentin	34	16	351	53700	5.06
16	P10719	ATP synthase subunit beta, mitochondrial	62	22	2820	56318	5.19
16	P69897	Tubulin beta-5 chain	23	8	243	49639	4.78
16	Q6P9T8	Tubulin beta-4B chain	19	7	163	49769	4.79
16	P85108	Tubulin beta-2A chain	13	5	118	49875	4.78
17	P31000	Vimentin	56	27	890	53700	5.06
17	P10719	ATP synthase subunit beta, mitochondrial	30	7	313	56318	5.19
18	P10719	ATP synthase subunit beta, mitochondrial	45	17	630	56318	5.19
18	P31000	Vimentin	31	14	445	53700	5.06
18	Q63081	Protein disulfide-isomerase A6	22	8	358	48143	5
19	Q68FY0	Cytochrome b-c1 complex subunit 1, mitochondrial	22	10	633	52815	5.57
19	P60711	Actin, cytoplasmic 1	18	7	171	41710	5.29
20	P60711	Actin, cytoplasmic 1	42	12	478	41710	5.29
20	P62738	Actin, aortic smooth muscle	32	10	226	41982	5.23
21	P60711	Actin, cytoplasmic 1	56	16	1639	41710	5.29
21	P62738	Actin, aortic smooth muscle	24	9	522	41982	5.23
22	P60711	Actin, cytoplasmic 1	53	15	1317	41710	5.29
22	P62738	Actin, aortic smooth muscle	24	9	531	41982	5.23
23	Q68A21	Transcriptional activator protein Pur-beta	3	2	55	33398	5.35
27	P55260	Annexin A4	26	8	91	35826	5.31
28	P54313	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	55	12	664	37307	5.6

28	P54311	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	40	10	597	37353	5.6
29	P37397	Calponin-3	19	4	36	36412	5.47
30	P37397	Calponin-3	10	3	59	36412	5.47
32	P19945	60S acidic ribosomal protein P0	46	13	443	34194	5.91
36	P19945	60S acidic ribosomal protein P0	45	24	259	34194	5.91
38	P04764	Alpha-enolase	11	5	61	47098	6.16
39	P15999	ATP synthase subunit alpha, mitochondrial	39	20	353	59717	9.22
39	P10719	ATP synthase subunit beta, mitochondrial	28	12	266	56318	5.19
39	B0BNF1	Septin-8	4	3	35	51220	5.74
40	B0BNF1	Septin-8	15	6	100	51220	5.74
41	P11598	Protein disulfide-isomerase A3	37	19	396	56588	5.88
41	P63039	60 kDa heat shock protein, mitochondrial	24	9	101	60917	5.91
42	P04764	Alpha-enolase	43	15	197	47098	6.16
45	B3GNI6	Septin-11	21	8	218	49663	6.24
46	P10860	Glutamate dehydrogenase 1, mitochondrial	34	16	225	61377	8.05
46	B3GNI6	Septin-11	10	4	68	49663	6.24
47	Q91Y81	Septin-2	22	6	40	41566	6.15
49	Q6AY23	Pyrroline-5-carboxylate reductase 2	3	1	73	33652	7.67
50	Q07936	Annexin A2	2	1	50	38654	7.55
51	Q07936	Annexin A2	35	12	486	38654	7.55
51	P04797	Glyceraldehyde-3-phosphate dehydrogenase	22	7	251	35805	8.14
52	P48679	Prelamin-A/C	50	31	1538	74279	6.54

53	P48679	Prelamin-A/C	44	28	1636	74279	6.54
54	P48679	Prelamin-A/C	52	34	1857	74279	6.54
55	P48679	Prelamin-A/C	47	29	1382	74279	6.54

[a] Swiss-Prot accession number.

[b] Calculated molecular weight.

[c] Calculated pI.

Proteins colored in red in this Table are commonly identified in immunoaffinity capture/LC-MS/MS (Supplementary Table S1).